

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Vinkemeier, Uwe
Darnell, Jr., James E.

(ii) TITLE OF INVENTION: PURIFIED STAT PROTEINS AND METHODS OF
PURIFYING THEREOF

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
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Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-182 N

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) IMMEDIATE SOURCE:
(B) CLONE: Human Stat91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
1 5 10 15
Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
20 25 30
Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
35 40 45
Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
50 55 60

Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
 115 120 125
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
 145 150 155 160
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175
 Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
 210 215 220
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
 245 250 255
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
 260 265 270
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
 275 280 285
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
 290 295 300
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315 320
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser

420	425	430	
Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu			
435	440	445	
Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu			
450	455	460	
Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu			
465	470	475	480
Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala			
485	490	495	
Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg			
500	505	510	
Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly			
515	520	525	
Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys			
530	535	540	
Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser			
545	550	555	560
Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly			
565	570	575	
Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys			
580	585	590	
Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg			
595	600	605	
Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly			
610	615	620	
Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser			
625	630	635	640
Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala			
645	650	655	
Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp			
660	665	670	
Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro			
675	680	685	
Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr			
690	695	700	
Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr			
705	710	715	720
Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg			
725	730	735	
Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val			
740	745	750	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
 1 5 10 15
 Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
 20 25 30
 Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
 35 40 45
 Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
 50 55 60
 Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
 115 120 125
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
 145 150 155 160
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175
 Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
 210 215 220
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
 245 250 255
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
 260 265 270
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
 275 280 285
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
 290 295 300
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315 320

Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
 420 425 430
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
 435 440 445
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
 450 455 460
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu
 465 470 475 480
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala
 485 490 495
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
 500 505 510
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly
 515 520 525
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
 530 535 540
 Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro

675	680	685
Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr		
690	695	700
Glu Leu Ile Ser Val Ser Glu Val		
705	710	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

11) SEQUENCE 1
 Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser Lys Val Arg
 1 5 10 15
 Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile Lys Ser Leu
 20 25 30
 Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr Leu Gln Asn
 35 40 45
 Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln Lys Gln Glu
 50 55 60
 Gln Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn Lys Arg Lys
 65 70 75 80
 Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr Glu Leu Thr
 85 90 95
 Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys Arg Arg Gln
 100 105 110
 Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu Asp Gln Leu
 115 120 125
 Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln Val Arg Gln
 130 135 140
 Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr Tyr Glu His
 145 150 155 160
 Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg Thr Phe Ser
 165 170 175
 Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu Arg Gln Pro
 180 185 190
 Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys Thr Gly Val
 195 200 205

Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln Glu Leu Asn
 210 215 220
 Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val Asn Glu Arg
 225 230 235 240
 Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly Thr His Thr
 245 250 255
 Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu Ala Ala Glu
 260 265 270
 Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly Thr Arg Thr
 275 280 285
 Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser Leu Ser Phe
 290 295 300
 Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu Glu Thr Thr
 305 310 315 320
 Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu Pro Ser Gly
 325 330 335
 Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu Pro Arg Asn
 340 345 350
 Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala Gln Leu Ser
 355 360 365
 Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg Gly Leu Asn
 370 375 380
 Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly Pro Asn Ala
 385 390 395 400
 Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys Glu Asn Ile
 405 410 415
 Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser Ile Leu Glu
 420 425 430
 Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly Cys Ile Met
 435 440 445
 Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys Asp Gln Gln
 450 455 460
 Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg Glu Gly Ala
 465 470 475 480
 Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly Glu Pro Asp
 485 490 495
 Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser Ala Val Thr
 500 505 510
 Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala Glu Asn Ile
 515 520 525
 Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp Lys Asp His
 530 535 540
 Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro Glu Pro Met
 545 550 555 560
 Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile

565

570

575

Ser Val Ser Glu Val His
580

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
1 5 10 15

Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
20 25 30

Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
35 40 45

Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
50 55 60

Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
65 70 75 80

His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
85 90 95

Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
100 105 110

Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
115 120 125

Asn Ile Gln
130

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGTCTCACT	GGTACGAACT	TCAGCAGCTT	GAACCAAAT	TCCTGGAGCA	GGTCACCAAG	60
CTTTATGATG	ACAGTTTCC	CATGGAAATC	AGACAGTACC	TGGCACAGTG	GTTAGAAAAG	120
CAAGACTGGG	AGCACGCTGC	CAATGATGTT	TCATTTGCCA	CCATCCGTTT	TCATGACCTC	180
CTGTCACAGC	TGGATGATCA	ATATAGTCGC	TTTTCTTTGG	AGAATAACTT	CTTGCTACAG	240
CATAACATAA	GGAAAAGCAA	GCGTAATCTT	CAGGATAATT	TTCAGGAAGA	CCCAATCCAG	300
ATGTCTATGA	TCATTTACAG	CTGTCTGAAG	GAAGAAAGGA	AAATTCTGGA	AAACGCCAG	360
AGATTTAAC	AGGCTCAGTC	GGGAAATATT	CAG			393

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAATTCCA TATGAGCACA GTGATGTTAG ACAAAC

36

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGATCCTAT TAGTGAACCT CAGACACAGA AATC

34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCACAGTGA	TGTTAGACAA	ACAGAAAGAG	CTTGACAGTA	AAGTCAGAAA	TGTGAAGGAC	60
AAGGTTATGT	GTATAGAGCA	TGAAATCAAG	AGCCTGGAAG	ATTTACAAGA	TGAATATGAC	120
TTCAAATGCA	AAACCTGCA	GAACAGAGAA	CACGAGACCA	ATGGTGTGGC	AAAGAGTGAT	180
CAGAAACAAG	AACAGCTGTT	ACTCAAGAAG	ATGTATTTAA	TGCTTGACAA	TAAGAGAAAG	240
GAAGTAGTTC	ACAAAATAAT	AGAGTTGCTG	AATGTCACTG	AACTTACCCA	GAATGCCCTG	300
ATTAATGATG	AACTAGTGGA	GTGGAAGCGG	AGACAGCAGA	GCGCCTGTAT	TGGGGGGCCG	360
CCCAATGCTT	GCTTGGATCA	GCTGCAGAAC	TGGTTCACTA	TAGTTGCGGA	GAGTCTGCAG	420
CAAGTTCGGC	AGCAGCTAA	AAAGTTGGAG	GAATTGGAAC	AGAAATACAC	CTACGAACAT	480
GACCCTATCA	CAAAAAACAA	ACAAGTGTAA	TGGGACCGCA	CCTTCAGTCT	TTTCCAGCAG	540
CTCATTCTAGA	GCTCGTTGT	GGTGGAAAGA	CAGCCCTGCA	TGQCAACGCA	CCCTCAGAGG	600
CCGCTGGTCT	TGAAGACAGG	GGTCCAGTTC	ACTGTGAAGT	TGAGACTGTT	GGTGAAATTG	660
CAAGAGCTGA	ATTATAATT	GAAAGTCAAA	GTCTTATTTG	ATAAAGATGT	GAATGAGAGA	720
AATACAGTAA	AAGGATTAG	GAAGTTCAAC	ATTTTGGCA	CGCACACAAA	AGTGATGAAC	780
ATGGAGGAGT	CCACCAATGG	CAGTCTGGCG	GCTGAATTTC	GGCACCTGCA	ATTGAAAGAA	840
CAGAAAAATG	CTGGCACCAAG	AACGAATGAG	GGTCCTCTCA	TCGTTACTGA	AGAGCTTCAC	900
TCCCTTAGTT	TTGAAACCCA	ATTGTGCCAG	CCTGGTTTGG	TAATTGACCT	CGAGACGACC	960
TCTCTGCCCG	TTGTGGTGAT	CTCCAACGTC	AGCCAGCTCC	CGAGCGGTTG	GGCCTCCATC	1020
CTTTGGTACA	ACATGCTGGT	GGCGGAACCC	AGGAATCTGT	CCTTCTTCCT	GACTCCACCA	1080
TGTGCACGAT	GGGCTCAGCT	TTCAGAACTG	CTGAGTTGGC	AGTTTCTTC	TGTCACCAAA	1140
AGAGGTCTCA	ATGTGGACCA	GCTGAACATG	TTGGGAGAGA	AGCTTCTTGG	TCCTAACGCC	1200
AGCCCCGATG	GTCTCATTCC	GTGGACGAGG	TTTGTAAAGG	AAAATATAAA	TGATAAAAAT	1260
TTTCCCTTCT	GGCTTGGAT	TGAAAGCATC	CTAGAACTCA	TTAAAAAACAA	CCTGCTCCCT	1320
CTCTGGAATG	ATGGGTGCAT	CATGGGCTTC	ATCAGCAAGG	AGCGAGAGCG	TGCCCTGTTG	1380
AAGGACCAGC	AGCCGGGGAC	CTTCCTGCTG	CGGTCAGTG	AGAGCTCCCG	GGAAGGGGCC	1440
ATCACATTCA	CATGGGTGGA	GCGGTCCCAG	AACGGAGGCG	AACCTGACTT	CCATGCGGTT	1500
GAACCCTACA	CGAAGAAAGA	ACTTTCTGCT	GTTACTTCC	CTGACATCAT	TCGCAATTAC	1560
AAAGTCATGG	CTGCTGAGAA	TATTCTGAG	AATCCCCTGA	AGTATCTGTA	TCCAAATATT	1620
GACAAAGACC	ATGCCTTGG	AAAGTATTAC	TCCAGGCCAA	AGGAAGCACC	AGAGCCAATG	1680
GAACTTGATG	GCCCTAAAGG	AACTGGATAT	ATCAAGACTG	AGTTGATTTC	TGTGTCTGAA	1740
GTTCAC						1746

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid